

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 9, 2002, 09:30:18 ; Search time 54 Seconds
(without alignments)
1896.853 Million cell updates/sec

Title: US-09-765-034-2
Perfect score: 1747
Sequence: 1 MGIAMNATCKMTLAAEA.....KSLTFSRMAHELLSFRK 334

Scoring table:
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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4	368.5	21.1	1020	3	US-08-513-974B-370
5	358.5	20.5	984	3	US-08-513-974B-57
6	358.5	20.5	1023	3	US-08-513-974B-379
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9	355	20.3	1842	1	US-08-446-088A-1
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15	345	19.7	1200	5	PCT-US92-02977-1	Sequence 1, Appli
16	342	19.6	2055	1	US-08-487-748A-3	Sequence 3, Appli
17	342	19.6	2055	3	US-08-480-070C-3	Sequence 3, Appli
18	342	19.6	2055	3	US-08-829-525-3	Sequence 3, Appli
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21	342	19.6	2055	4	US-09-310-367-3	Sequence 3, Appli
22	342	19.6	2055	4	US-09-032-337-3	Sequence 3, Appli
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25	338	19.3	1200	5	PCT-US95-03032-1	Sequence 1, Appli
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27	338	19.3	1748	1	US-08-202-056-8	Sequence 4, Appli
28	338	19.3	1901	1	US-08-153-848-43	Sequence 8, Appli
29	338	19.3	1901	3	US-09-299-843A-43	Sequence 43, Appli
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31	338	19.3	1901	5	PCT-US93-11153-43	Sequence 43, Appli
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36	333.5	19.1	1255	1	US-08-476-000-3	Sequence 3, Appli
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43	331	18.9	1883	1	US-08-202-056-2	Sequence 1, Appli
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45	331	18.9	1933	1	US-08-410-451-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-559-524A-1
; Sequence 1, Application US/08559524A
; Patent No. 5871963
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,524A
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044481-5010-00-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1996 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 625..1626
 US-08-559-524A-1

Alignment Scores:
 Pred. No.: 5.62e-176 Length: 1996
 Score: 1725.00 Matches: 331
 Percent Similarity: 99.10% Conservative: 0
 Best Local Similarity: 99.10% Mismatches: 3
 Query Match: 98.74% Indels: 0
 DB: 2 Gaps: 0

US-09-765-034-2 (1-334) x US-08-559-524A-1 (1-1996)

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 QY 21 LeuGluysTYTYrLeuSerIlePheTYrGlyIleGluPheValIaGlyValLeuGly 40
 DB 685 CTGGAAGAAGTACTACCTTTCATTTTATGGAGTTGAGTTCGTTGGAGGCTCTTGA 744
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 DB 745 AATACCATTTGTTGTTAGCGCTACATCTTCTCTGGAAGAACTGGACAGCAGTAATATT 804
 QY 61 TyrrleupheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIle 80
 DB 805 TATCTCTTAACTCTCTGCTGACTTACCTTTCTGTGCACCCCTCCCATGCTGATA 864
 QY 81 ArgSerTYrAlaAsnGlyAsnTPrIleTYrGlyAspValLeuCysIleSerAsnArgTYr 100
 DB 865 AGGAGTTATGCGCATGGAATGATGATATGAGAGCGCTGCTGATAGCAACCGATAT 924
 QY 101 ValLeuHisAlaAsnLeuTYrThrSerIleLeuPheLeuThrPheIleSerIleAspArg 120
 DB 925 GTGCTTCATGCGCAACCTTATACAGCAGCATCTCTTCTCATCTTATACGATGATGCA 984
 QY 121 TyrrleuIleIleLysTYrProPheArgGluHisLeuGluInLysGluPheAlaIle 140
 DB 985 TACTTGATATTAAGTATCCTTTCGAGAACACCTTTCGCAAAAGAAAGAACTTGTCTATT 1044
 QY 141 LeuIleSerLeuAlaIleTPrValLeuValIleThrLeuGluLeuLeuProIleLeuProLeu 160
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 QY 161 IleAsnProValIleIleHisAspAsnGlyThrCysAsnAspPheAlaSerSerGlyAsp 180
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 QY 181 ProAsnTYrAsnLeuIleTYrSerMetCysLeuThrLeuGluPheLeuIleProLeu 200
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QY 281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValIlePheTYrPheLeuGluAsp 300
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 QY 301 HisPheArgAspMetLeuMetLeuAsnGluIleuArgHisAsnPheLysSerLeuThrSerPhe 320
 DB 1525 CACTTCAGGAGCATGCTGATGATGAACTGAGACCAACTTCATAATCCCTTACATCTT 1584
 QY 321 SerArgTPrAlaHisGluLeuLeuLeuSerPheArgGluLys 344
 DB 1585 AGCAGATGGCTCATGAACTCTTACTTTCATTCAGAGAAAG 1626

RESULT 2

US-08-749-707-1
 Sequence 1, Application US/08749707
 Patent No. 6063582

GENERAL INFORMATION:

APPLICANT: Conley, Pamela B.
 APPLICANT: Janlzen, Hans-Michael
 TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
 STREET: 1800 M Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20036-5869

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/749,707
 FILING DATE: 15-NOV-1996
 CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Adler, Reid G.
 REGISTRATION NUMBER: 30,988
 REFERENCE/DOCKET NUMBER: 044481-5010-01-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-467-7000
 TELEFAX: 202-467-7176

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1996 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:

NAME/KEY: CDS
 LOCATION: 625..1626
 US-08-749-707-1

Alignment Scores:

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 DB: 3 Gaps: 0

US-09-765-034-2 (1-334) x US-08-749-707-1 (1-1996)

QY 1 MetleuglylIleMetAlaTPAsnAlaThrCysLysAsnTPLeuAlaIaIaAla 20
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 QY 21 LeuGluysTYTYrLeuSerIlePheTYrGlyIleGluPheValIaGlyValLeuGly 40
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 Db 1225 TTGTGATGTTGTTCTTTATTTACAGATGCTCTCTCTTAAGCAGAGGAATAGGACAG 1284
 Qy 221 ValAlaThrAlaLeuProLeuGlnLysProLeuAsnLeuValIleMetAlaValIle 240
 Db 1285 GTTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1344
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 Db 1405 GGGAGTGGAGAGCATATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1464
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 Db 1465 CGGGCTTTGGGCTTCTGGAAGTGCATGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTG 1524
 Qy 301 HisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheLysSerLeuThrSerPhe 320
 Db 1525 CACTTACAGGACATGCTGATGATCAATCAATGAGACAACTCAAACTCCCTTACATCTCT 1584
 Qy 321 SerArgTyrAlaHisGluLeuLeuLeuSerPheArgGlnLys 334
 Db 1585 AGCAGATGGGCTCATGACTCCCTACTTCTCATTCAGAGAAAG 1626

TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
 NUMBER OF SEQUENCES: 380
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/513,974B
 FILING DATE: 14-SEP-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP95/01599
 FILING DATE: 10-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-093989
 FILING DATE: 19-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-057186
 FILING DATE: 16-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-007177
 FILING DATE: 20-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-326611
 FILING DATE: 28-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-270017
 FILING DATE: 02-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236357
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236356
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189274
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189273
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189272
 FILING DATE: 11-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Resnick, David S.
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 45753
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 41:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 984 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-513-974B-41
 Alignment Scores:
 Pred. No.: 1,42e-30 Length: 984
 Score: 368.50 Matches: 96
 Percent Similarity: 48.58% Conservative: 58
 Best Local Similarity: 30.28% Mismatches: 128


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FEATURE:
; NAME/KEY: CDS
; LOCATION: 28..1011
US-08-513-974B-370

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Score: 368.50      Matches: 96
Percent Similarity: 48.58%      Conservative: 58
Best Local Similarity: 30.28%      Mismatches: 128
Query Match: 21.09%      Indels: 35
DB: 3      Gaps: 8

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QY 82 SerTyrAlaAsnGly--AsnTrpIleTyrGlyAspValLeuLysIleSerAsn 100
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QY 140 IleLeuIleSerLeuAlaIleTrpValLeuValThrLeuLysLeuProIleLeu 159
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DB 460 TGGGTAGTGTGTGGAGTGTGTGGCTGCTGACAGCCAGTGGCTGCCAGCGCAG 519
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QY 160 LeuIleAsnProValIleThrAspAsnGlyThrCysAsnAspPheIleSer 179
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DB 520 TTTGTGCCACAGACGATCCAGCGCAACCGCATGCTGCTACGACCTGAGCC 579
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QY 180 AspProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLeuLysGlyPheLeu 199
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DB 580 CTGTCTACTGCTACCTGCGCTATGATGATGCGCTCAACGCTATCGGCTTGTG 639
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QY 200 LeuPheValMetCysPhePheTyrTyrLysIleAlaLeuPheLysGlnArg 219
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DB 640 TTCATAGCCCTTACTGGCTGTGTATGTGCGATGCGC-----GCGCCGCTG 690
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QY 220 GluValAlaThrAlaLeuProLeu-----GluLysProLeuAsnLeuVal 234
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QY 235 IleMetAlaValAlaIlePheSerValProPheThrProTyrHisValMetArg 254
    :::::  |||||  :::::  |||||  :::::  |||||  :::::  |||||
DB 751 GTGTGTGTGGCAGCTGTGTGGCATAGCTTGTGCTTTCACATCACCAGACAGCC 810
    :::::  |||||  :::::  |||||  :::::  |||||  :::::  |||||
QY 255 ArgIleAlaSerArgLeuGlySerTrpLysGlnTyrGlnCysThrGlnValIle 274
    :::::  |||||  :::::  |||||  :::::  |||||  :::::  |||||
DB 811 TACTTGGCTGTGGC-----TCCAGCGCCGCGTCTCTTGGCCCT-----G 858
    :::::  |||||  :::::  |||||  :::::  |||||  :::::  |||||
QY 275 SerPhe-----TyrIleValIleThrArgProLeuAlaPheLeuAsnSerVal 291
    :::::  |||||  :::::  |||||  :::::  |||||  :::::  |||||
DB 859 ACCTTGTGCTGCTACCAAGGCACTGCGCCCTTCGCGAGTCAACAGTGTTCGGAC 918
    :::::  |||||  :::::  |||||  :::::  |||||  :::::  |||||
QY 292 ProValPheTyrPheTyrLeuLeuGlyAspHisPheArgAspMetLeuMetAsn 311
    :::::  |||||  :::::  |||||  :::::  |||||  :::::  |||||

```

```

DB 919 CCCATTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 954
QY 312 HisAsnPheLysSerLeuThrSerPheSerArgTrpAlaHisGluLeu 328
    :::::  |||||  :::::  |||||  :::::  |||||  :::::  |||||
DB 955 -----CGGCAACCCGACGATCTCTTA 975
    :::::  |||||  :::::  |||||  :::::  |||||  :::::  |||||

RESULT 5
US-08-513-974B-57
; Sequence 57, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hituma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiko
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513, 974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753

```


PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 379:
SEQUENCE CHARACTERISTICS:
LENGTH: 1023 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 37..1020
US-08-513-974B-379

Alignment Scores:
Pred. No.: 1,79e-29 length: 1023
Score: 358.50 Matches: 96
Percent Similarity: 46.67% Conservative: 51
Best Local Similarity: 30.48% Mismatches: 133
Query Match: 20.52% Indels: 35
Gaps: 8

US-09-765-034-2 (1-334) x US-08-513-974B-379 (1-1023)

QY 30 TyrGlyIleGluPheValAlaGlyValLeuGlyAsnThrIleValTyrGlyTyrIle 49
Db 133 TATTGGCGGCTGCTGGCGGCTGCGCTGACATGTCATGTATACAGATCGC 192
QY 50 PheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsnLeuSerValSerAsp 69
Db 193 ACGTCCCGCGGCGCTGACCCGCGCGCGCTGACACCTTAACCTTGCTGGCTGAC 252
QY 70 LeuAlaPheLeuGlyThrLeuPheMetLeuIleArgSerTyrAlaAsnGly---AsnTrp 88
Db 253 CTGCTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 312
QY 89 IleTyrGlyAspValLeuGlyLysSerAsnArgTyrValLeuHisAlaAsnLeuTyrThr 108
Db 313 CCTTTGGGAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 372
QY 109 SerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIleIleIleTyrProPhe 128
Db 373 AGCATGCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
QY 129 ArgGlu---HisLeuLeuGlnLysGluPheAlaIleLeuIleSerLeuAlaIleTrp 147
Db 433 GCCCCTGGCACAACGCTGGGGGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 492
QY 148 ValLeuValThrLeuGluLeuLeuProIleLeuProIleLeuAsnProValIleThrAsp 167
Db 493 CTGGCGGTGACAAACGAGTCCGCTGCCACAGCATCTGCTGCTGCCACAGCATCCAGCT 552
QY 168 AsnGlyThrThrLysAsnAspPheAlaSerSerGlyAspProAsnTyrAsnLeuIleTyr 187
Db 553 AACCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 612
QY 188 SerMetCysLeuThrLeuGlnGlyPheLeuIleProLeuPheValMetCysPhePheTyr 207
Db 613 GGCATGGCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 672
QY 208 TyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaThrAlaLeuProLeu 227
Db 673 TGTCTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 723
QY 228 Glu-----LysProLeuAsnLeuValIleMetAlaValValIlePheSer 242

Db 724 GCCCAGAGCGGCTGGCAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 783
QY 243 ValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySer 262
Db 784 ATGAGCTTCTGCTGCTTTCATCATTCCACAGACAGCTACTGCA-----GTGGCTCG 837
QY 263 TrpLysGlnTyrGlnCysThrGlnValAlaIleAsnSerPhe-----TyrIleVal 279
Db 838 ACGCGGCGCTGCCCTGCACT-----GTAATGAGGCGCTTTCAGCGGCGCTCAAAAGCG 891
QY 280 ThrArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuGly 299
Db 892 ACGCGCGCTTTCAGCTGCGCAACAGCGCTGCGACCCCACTCCTCTACTACACCGAC 951
QY 300 AspHisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheLysSerLeuThrSer 319
Db 952 AAGAGTTCCG----- 963
QY 320 PheSerArgTrpAlaHisGlnLeuLeuLeuSerPheArgGluLys 334
Db 964 -----CGCGGACCATGAGCTCTACAGAACTCAGACGCAAA 1002

RESULT 7
US-08-442-134A-1
Sequence 1, Application US/08442134A
Patent No. 5596088
GENERAL INFORMATION:
APPLICANT: Boucher, Richard C.
APPLICANT: Weisman, Gary A.
APPLICANT: Turner, John T.
APPLICANT: Harden, Thomas K.
APPLICANT: Parr, Claude E.
APPLICANT: Sullivan, Daniel M.
APPLICANT: Erb, Laura
APPLICANT: Lustig, Kevin D.
TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
TITLE OF INVENTION: Null Cells Expressing P2U Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5596088th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,134A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sidley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-71A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1842 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 57..1181
US-08-442-134A-1

QY 311 ArgHisAsnPheIysSerLeuThrSerPheSerArgTrpAlaHisCLeuLeuLeuSer 330
DB 928 -----CGGCGAGCACATGAGTCTCTACAGAAA 954
QY 331 PheArgGLuLys 334
DB 955 CTCACAGACAAA 966

RESULT 11
US-09-044-404A-1
; Sequence 1, Application US/09044404A
; Patent No. 6200775
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: HALSEY, WENDY
; APPLICANT: ELLIS, CATHERINE
; APPLICANT: AMES, ROBERT
; APPLICANT: FOLEY, JAMES
; APPLICANT: SARAU, HENRY
; TITLE OF INVENTION: CDNA CLONE HMTMB1 THAT ENCODES
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 790 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,404A
; FILING DATE: MARCH 19, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/844,795
; FILING DATE: APRIL 22, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T.
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: GH-70001-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1578 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-044-404A-1

Alignment Scores:
Pred. No.: 1.15e-28 Length: 1578
Score: 353.50 Matches: 91
Percent Similarity: 47.52% Conservative: 62
Best Local Similarity: 28.26% Mismatches: 152
Query Match: 20.23% Indels: 17
DB: 4 Gaps: 8

US-09-765-034-2 (1-334) x US-09-044-404A-1 (1-1578)
QY 8 AsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaLeuGluLysTrpLeuSer 27
DB 497 TCTGCCACATGCGCATGACTATT-----GATGACTTCGCGCAATCAAGTGTATTCC 547

QY 28 IlePheTyGlyIleGluPheValValGlyValLeuGlyAsnThrIleValValTyGly 47
DB 548 ACCCTGTACTCATGATCTCTGTGTAGGCTTCTTGCGAATGGCTTGTCTGTATGTC 607
QY 48 TyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsnLeuSerVal 67
DB 608 CTCATATAAAACCTATCACAAGAAAGTCAGCCTTCCAAAGTATACATGATTATTAATGACGTA 667
QY 68 SerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAlaAsn---Gly 86
DB 668 GCAGATCTACTTGTGTGTGACACATGCGCTCTCGTGTGTGTATATGTCACAAAGG 727
QY 87 AsnTrpIleTyrGlyAspValLeuGlyIleSerAsnArgTyrValLeuHisAlaAsnLeu 106
DB 728 ATTTGGCTCTTGTGATCTCTTGTGCGCTCAGACCATTCCTTGTATGTCACACCTC 787
QY 107 TyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIleIleLysTyr 126
DB 788 TATTGTAGCATCTTCTTATGACAGCCATGAGCTTTTCCGGTGCATTGCAATTGCTTTT 847
QY 127 ProPheArgGluHisLeuLeuGlnLysGluPheAlaIleLeuIleSerLeuAlaIle 146
DB 848 CCAGTCCAGAACATTAATTGGTTACACAGAAAAGCCAGTTGTGTGTAGGTATT 907
QY 147 TrpValLeuValThrLeuGluLeuProIleLeuProLeuIleAsnProValIleThr 166
DB 908 TGGATTTTGTGATTTTGACACAGTCTCCATTTCTATGCGCAACACAAAAGATGG 967
QY 167 AspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAsp-----ProAsnTyr 183
DB 968 AAAAATAATACCAAGTGC-----TTTGAGCCCCCACAAGACATCAAACTAAATAATCAT 1021
QY 184 AsnLeuIleTyrSerMetCysLeuThrLeuGlyPheLeuIlePro-----LeuPhe 201
DB 1022 GTTTGGTCTGTGATATGATGTCATTTGTTGGCTTATATCCCTTTTGTATTATA 1081
QY 202 ValMetCysPhePheTyrTyrIleAlaLeuPheLeuLysGlnArgAsnArgGlnVal 221
DB 1082 ATGTCTGTACCAATGATCATCTTGTACCTTCTAAATAAATCAATGAAAAAATCTG 1141
QY 222 AlaThrAlaLeuProLeuGlnLysProLeuAsnLeuValIleMetAlaValIlePhe 241
DB 1142 TCAGATCAT-----AAAAAGGCTATAGATGATGATGCTGACCGCTGCTTT 1192
QY 242 SerValProPheThrProTyrHisValMetArgAsnValArgIleAsnArgLeuGly 261
DB 1193 TTAGTCAGTTTCAATGCGATATCATATTCAAGCATTCACCTTCAATTTTACACAT 1252
QY 262 SerTrpLysGlnTyrGlnCysThrGlnValVal---IleAsnSerPheTyrIleValThr 280
DB 1253 GAACCTAAA-----CCCTGTGATCTGCTTGAAGATGAGAAAGTCCGATGATTAAC 1306
QY 281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAsp 300
DB 1307 TTGTCTGTGCGTCATCCATTCATTTGCTTGTGACCCCTGCTATATTTCTTTCTGGGGCT 1366
QY 301 HisPheArgAspMetLeuLeuAsnGlnLeuArgHisAsnPheLysSerLeuThrSerPhe 320
DB 1367 AACTTTAGGAAGAGCGTGTCTACATTTAGAAAGCATTTCTTGCCAGCGTACTTATGTA 1426
QY 321 SerArg 322
DB 1427 CCCAGA 1432

RESULT 12
US-08-383-750-3
; Sequence 3, Application US/08383750
; Patent No. 5744301
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; APPLICANT: Kieff, Elliot
; TITLE OF INVENTION: Epstein Barr Virus Induced Genes
; NUMBER OF SEQUENCES: 8


```

: TELEPHONE: 617-720-3500
: TELEFAX: 617-720-2441
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 1643 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: double
:   TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: FEATURE:
:   NAME/KEY: CDS
:   LOCATION: 34..1116
: US-08-352-678-3

Alignment Scores:
Pred. No.: 4,766-28      Length: 1643
Score: 348.00           Matches: 95
Percent Similarity: 49.55% Conservative: 69
Best Local Similarity: 28.70% Mismatches: 135
Query Match: 19.92%      Indels: 32
DB: 3                   Gaps: 10

US-09-765-034-2 (1-334) x US-08-352-678-3 (1-1643)
QY 15 LeuAlaAlaGluAlaAlaLeuGluLysTyrTyrLeuSerIlePheTyrGlyIleGluPhe 34
DB 100 CTTCTAGACATACACACGCGGAGATAGTAATGCCCTCTGCATTAACGCTCGCTTC 159
QY 35 ValValGlyValLeuGlyLysThrIleValValTyrGlyTyrIlePheSerIleLysAsn 54
DB 160 ATCATTTGGCTGTGGGAAACTTACTAGCCTTGCTGCTATTGTTAAACAGCAAAAA 219
QY 55 TTPAsnSerSerAsnIleTyrLeuPheAsnLeuSerValSerAspLeuAlaPheLysCys 74
DB 220 ATCACTCTACACACCTCTATTAACAACAATTTGCTGATTTCTGATTAATCTTTTACAG 279
QY 75 ThrLeuProMetLeuIleArgSerTyrAlaAsnGly---AsnTrpIleTyrGlyAspVal 93
DB 280 GCTTTGGCTACACAGATACCTACTAGTCAATGGCTTTGAGCGCAATCGAGATGCC 339
QY 94 LeuCysIleSerAsnArgTyrValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeu 113
DB 340 TTGTGTAGATTAACCTGCTAGTGTTTTACATCAACACATATGACAGGTGTGAATTATG 399
QY 114 ThrPheIleSerIleAspArgTyrLeuIleIleLysTyrTyrPheArgLysHisLeuLeu 133
DB 400 ACCTGCTGATGATGACCGCTTCAATGCTGTGGTGCACCTCTAGCTACACAAGATA 459
QY 134 GlnLysLysGlnPheAlaIleLeuIleSerLeuAlaIleTrpValLeuValThrLeuGlu 153
DB 460 AAAAGGATTGAACATGCAAAAGCGGTGTCATATTGCTGTGATTTCTAGATTGCTCAG 519
QY 154 LeuLeuProIleLeuProLeuIleAsnProValIleThrAspAsnGly-----ThrThr 171
DB 520 ACACTGCCACTC-----CTCATCAACCTTATGTCAAAAGCAGAGGCTGAAGATTACA 573
QY 172 CysAsnAspPheAlaSerSerGlyAspProAsnTyrAsnLeuIleTyrSerMetCysLeu 191
DB 574 TCCATGGAGATAT-----CCAAACTTGAAGAAACATTAATCTCTCTCCCTGG 618
QY 192 ThrLeuLeu-----GlyPheLeuIleProLeuPheValMetCysPhePhe 206
DB 619 AATTCGCTTGGGGGCGATTTTCATAGATGTGACTTCCCTATATATCATTCATCTGC 678
QY 207 TyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaIleThrAlaLeuPro 226
DB 679 TATTTCTCAATCTGCTGCAAACTCTTCAAGACTGCCAAACAA-----AACCCA 726
QY 227 Leu-----GlnLysProLeuAsnLeuValIleMetAlaValAl 239
DB 727 CTCACATGAGAAATCTGGTGTAAACAAAGGCTCTCAACACATATATCTTATTTATGTT 786
QY 240 IlePheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArg 259

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DB 787 GTGTTGTCTCTGTTTCAACCTTACCATGTGCAATTATTCAACATATGATTAGAAG 846
QY 260 LeuGlySerTrpLysGlnTyrGlnCysThrGlnValValIleAsnSerPheTyrIle--- 278
DB 847 CTTTCGTTCTCAATTTCTCTGGAATGTACCAA-----AGACATTGCTTCCAGATTCT 900
QY 279 -----ValThrArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPhe 296
DB 901 CTCGACTTACAGTATGCTGATGAAGCTTCAATGTCTGCATGACCCCTTTATCTACTTC 960
QY 297 LeuLeuGlyAspHisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheLys--- 315
DB 961 TTTGCATGTAAAGGATATAAGAGAAAGTTATGAGGATGCTGAAAGCGCAAGTCACTGA 1020
QY 316 SerLeuThrSerPheSerArgTrpPalaHisGlu 326
DB 1021 TCGATTCTAGTGTCTGTGAATGACGCCCTGAA 1053

RESULT 14
PCT-US93-09636-3
: Sequence 3, Application PC/TUS9309636
: GENERAL INFORMATION:
: APPLICANT: Birkenbach, Mark
: APPLICANT: Kieff, Elliot
: TITLE OF INVENTION: Epstein Barr Virus Induced Genes
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
:   ADDRESSER: Sterne, Kessler, Goldstein & Fox
:   STREET: 1100 New York Avenue N.W., Suite 600
:   CITY: Washington
:   STATE: D.C.
:   COUNTRY: U.S.A.
:   ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: PCT/US93/09636
:   FILING DATE: herewith
: CLASSIFICATION:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 371-2600
: TELEFAX: (202) 371-2540
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 1643 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: both
:   TOPOLOGY: linear
: FEATURE:
:   NAME/KEY: CDS
:   LOCATION: 34..1116
: PCT-US93-09636-3

Alignment Scores:
Pred. No.: 4,766-28      Length: 1643
Score: 348.00           Matches: 95
Percent Similarity: 49.55% Conservative: 69
Best Local Similarity: 28.70% Mismatches: 135
Query Match: 19.92%      Indels: 32
DB: 5                   Gaps: 10

US-09-765-034-2 (1-334) x PCT-US93-09636-3 (1-1643)
QY 15 LeuAlaAlaGluAlaAlaLeuGluLysTyrTyrLeuSerIlePheTyrGlyIleGluPhe 34
DB 100 CTTCTAGACATACACACGCGGAGATAGTAATGCCCTCTGCATTAACGCTCGCTTC 159
QY 35 ValValGlyValLeuGlyLysThrIleValValTyrGlyTyrIlePheSerIleLysAsn 54

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Db 160 ATCATTTGGGCTGGGAAACTTACTAGCCTTGTCGTCATTTCTTCAAAACAGAAAAA 219
Oy 55 TrpAsnSerSerAsnIleTyrIleuPheAsnLeuSerValSerAspLeuAlaPheLeuCys 74
Db 220 ATCAACTCTACACCCCTATATCAACAAATTTGGTATGATTCGATATATCTTTACACAG 279
Oy 75 ThrLeuProMetLeuIleArgSerTyrAlaAsnGly---AsnTyrIleTyrIleAspVal 93
Db 280 GCTTTGGCTACACGAAATACCTACTAGTACATGCAATGGCTTTGAGGAGGAAATCCGAGATGCC 339
Oy 94 LeuCysIleSerAsnArgTyrValLeuHsAlaAsnLeuTyrThrSerIleLeuPheLeu 113
Db 340 TTGCTAGAGATTAATCGCGTAGTGTATTACATCAACACATATGCAAGGTGTAACCTTTAG 399
Oy 114 ThrPheIleSerIleAspArgTyrIleuIleIleTyrTyrProPheArgGluHisLeuLeu 133
Db 400 ACCCTCCCTGAGATTTAGCCGCTTTCATGTGTGGTGACCCCTCTACGCTACAAAGATA 459
Oy 134 GluLysLysGluPheAlaIleLeuIleSerLeuAlaIleTyrValLeuValHisLeuGlu 153
Db 460 AAAAGGATTTGAACATGCAAAAGGCGTGTGCATATTTGTGTGATTTCTGATTTGCTCTAG 519
Oy 154 LeuLeuProIleLeuProLeuIleAsnProValIleThrAspAsnGly---ThrThr 171
Db 520 AACTCCCACTC-----CTCATCAACCCATGTCACAAAGCAGAGGCTGAAGATTTACA 573
Oy 172 CysAsnAspPheAlaSerSerGlyAspProAsnTyrAsnLeuIleTyrSerMetCysLeu 191
Db 574 TGCATGGAGTAT-----CCAACTTGAAGAACTAAATCTCTCTCCCTCG 618
Oy 192 ThrLeuLeu-----GlyPheLeuIleProLeuPheValMetCysPhePhe 206
Db 619 ATTCTGCTTGGGGCATGTTTCTATAGGATATGACTTCCATTAATCTTCTCATCTGC 678
Oy 207 TyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaThrAlaLeuPro 226
Db 679 TATTTCTGAGATCTGCTGCAACTCTTCAGAACTGCCAAACAA-----AACCA 726
Oy 227 Leu-----GluLysProLeuAsnLeuValIleMetAlaValVal 239
Db 727 CTCACGTGAAATCTGCTGTAAACAAAGGCTCTCAACACAAATATCTTATTTGTT 786
Oy 240 IlePheSerValProPheThrProTyrHisValMetArgAsnValArgIleLeuAsnArg 259
Db 787 GTGTTTGTCTCTGTTTACACCTTACCAATGTTGCAATTTATTCACATATGATTAGAG 846
Oy 260 LeuGlySerTyrLysGlnTyrGlnCysThrGlnValValIleAsnSerPheTyrIle--- 278
Db 847 CTTCGTTTCTGAATTTCTCGGAATGTAGCCAA-----AGACATTCGTTCCAGATTTCT 900
Oy 279 -----ValThrArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPhe 296
Db 901 CTGCATTTAGATGATGCTGATGAACTTCAATGCTGATGAGACCTTTTATCTACTTTC 960
Oy 297 LeuLeuGlyAspHisPheArgAspMetLeuMetAsnGlnLeuArgHisAsnPheLys--- 315
Db 961 TTTCATGTTAAAGGATTAAGAGAAAGGTATAGAGAGATGCTGAAGCGCAAGTCAAGTGA 1020
Oy 316 SerLeuThrSerPheSerArgTyrPheAlaHisGlu 326
Db 1021 TCGATTTCTAGTCGTGAGTCAAGCCCTGAA 1053

```

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STREET: 225 Franklin Street
City: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT-US92/02977
FILING DATE: 19920410
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/685,101
FILING DATE: April 10, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00231/051002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1200
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US92-02977-1

Alignment Scores:
Pred. No.: 6,36e-28 Length: 1200
Score: 345.00 Matches: 99
Percent Similarity: 44.02% Conservative: 63
Best Local Similarity: 26.90% Mismatches: 140
Query Match: 19.75% Indels: 66
DB: Gaps: 12

US-09-765-034-2 (1-334) x PCT-US92-02977-1 (1-1200)
Oy 1 MetLeuGlyIleMetAlaTrpAsnAlaThr---CysLysAsnTrpLeuAlaAlaGluAla 19
Db 105 GTAATGGAAGTAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 164
Oy 20 Ala----- 20
Db 165 GCAAAATGCTACTGCTATGCTCTCTGTAGAAAAAGATTATAGCCCTGTCTGTAGTCAAC 224
Oy 21 -----LeuGluLysTyrTyrIleuSerIlePheTyrGlyIleGluPheValValGlyVal 38
Db 225 CAGACACTTAACAAATATAGTGTGTGCTGCTCATATGCCCTGTCTCTCTGCTGACGCTG 284
Oy 39 LeuGlyAsnThrIleValValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSer 58
Db 285 CTGGCAACTCCCTGCTGATGCTGTGCTACTGATGACACCGGAGCAACCGTTGCGTCAAC 344
Oy 59 AsnIleTyrIleuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMet 78
Db 345 GACGTCTACCTGCTGAACCTGGCCGACGTCGCTTTTGGCTTACCATGCTATGCTATG 404
Oy 79 LeuIleArgSerTyrAlaAsnGlyAsnTrpIleTyrGlyIleAspValLeuCysIleSerAsn 98
Db 405 TGGCGCCGTCTCAAGCAAAAGC---TCGATTTTGGCGACGCCCTGTGCAAGGTGGGG 461
Oy 99 ArgTyrValLeuHsAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIle 118
Db 462 TCGCTTGTGAAGGAGTCACTTACAGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 521
Oy 119 AspArgTyrLeuIleIleIleTyrProPheArgGlnHisLeuGlnLysLysGluPhe 138

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RESULT 15
PCT-US92-02977-1
Sequence 1, Application PC/TUS9202977
GENERAL INFORMATION:
APPLICANT: Navario, Javier et al.
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTORS AND
RELATED MOLECULES AND
METHODS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson

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Db	522	GACCGTACCTGGGACATTGGCATGTACTGCGACA--CTGACCAGAAAGGCCACTTG	578
QY	139	AlaIleuIleSerLeuAlaIleTrrPvalLeuValThrLeuGluLeuProIleLeu	158
Db	579	GTCAGTTCATATGTCTGGGACACTGGGGCGTGCTCTGATTTGTCCCTGGCTTCTTC	638
QY	159	ProLeuIleAsnProValIleThrAspAsnGlyThr-----CysAsnAspHeaIa	176
Db	639	---CTCTTCGGCCAAAGCTTTTCTCCAAACATCTCAGCGCGGTGTGCTATGAGACCTG	695
QY	177	SerSerGlyAspProAsnTybAsnLeuIleTybSerMetCysLeuThrLeuLeuGlyHe	196
Db	696	GGTCACACACACAGCGAAATGGCCGATGCGTGGCGGATCTGCCACACACTTTCGGCTTC	755
QY	197	LeuIleProIleuHeuIleMet-----CysPhePheTybTybIleIleAlaIleuPheLeu	214
Db	756	ATCTCGCGCGTGGCTGGGACATGCTGTTTCTATAGGCTTACCCGTCGACGCTGTTCAG	815
QY	215	LysGlnArgAsnArgGlnValAlaThrAlaLeuProLeuGluLysProLeuAsnIleuVal	234
Db	816	GCCACATGGGGCGAGAG-----CACCGGGCCATGGGGGTATC	854
QY	235	IleMetAlaValValIlePheSerValProPheThrProTybHisValMetArgAsnVal	254
Db	855	TTTGGCGCTGTGGTCATCTTTCCTCTGCTGGCTGCCCTCAACACTG-----GTC	905
QY	255	ArgIleAlaSerArgLeuGlySerTrrPlysGlnTybGlnCysThcIleVal-----	272
Db	906	CTGTGTCGAACACCTTC-----ATGAGAACCGAGTGATCCAGAG	947
QY	273	-----IleAsnSerPheTybIleValThrArgProLeuAlaPhe	285
Db	948	ACGATGTCAGCGTCGCATATGCATTTAGCGGGCCCTGAGCCACAGAGATTCCTGGGCTTC	1007
QY	286	LeuAsnSerValIleAsnProValPheTybPheLeuLeuGlyAspHisPheArgAspMet	305
Db	1008	CTGACAGCTGCCCTCAACCCCATCATCTACGCTTCATTGGCCAAACATTTCGGCATGCA	1067
QY	306	LeuMetAsnGlnLeu-----ArgHisAsn	313
Db	1068	TTTCTCTCAAGATGCTGTGGCGCCCGGCTTATTAGCAGAGAGATTCCTGCACAGCATCGG	1127
QY	314	PheIysSerLeuThrSerPheSer	321
Db	1128	GTCACGCTTATACTTCTCTCTCT	1151

Search completed: December 9, 2002, 12:24:08
Job time : 74 secs

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